

RAW SEQUENCE LISTING

DATE: 12/11/2001

PATENT APPLICATION: US/09/042,488B

TIME: 10:26:16

Input Set : A:\SA1520-2.APP.txt

Output Set: N:\CRF3\12112001\I042488B.raw

1633
#32 145
12/31/01 1600

p.5

3 <110> APPLICANT: EVANS, RONALD M.
4 NO, DAVID
5 SAEZ, ENRIQUE
7 <120> TITLE OF INVENTION: METHODS FOR MODULATING EXPRESSION OF EXOGENOUS GENES IN
8 MAMMALIAN SYSTEMS, AND PRODUCTS REALTED THERETO
10 <130> FILE REFERENCE: SALK1520-2
12 <140> CURRENT APPLICATION NUMBER: 09/042,488B
13 <141> CURRENT FILING DATE: 1998-03-16
15 <150> PRIOR APPLICATION NUMBER: 08/974,530
16 <151> PRIOR FILING DATE: 1997-11-19
18 <150> PRIOR APPLICATION NUMBER: 08/628,830
19 <151> PRIOR FILING DATE: 1996-04-05
21 <160> NUMBER OF SEQ ID NOS: 18
23 <170> SOFTWARE: PatentIn Ver. 2.1
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 71
27 <212> TYPE: PRT
28 <213> ORGANISM: Artificial Sequence
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31 <223> OTHER INFORMATION: Description of Artificial Sequence: Consensus
32 peptide sequence
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37 <223> OTHER INFORMATION: Any amino acid
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41 <222> LOCATION: (5)..(6)
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52 <223> OTHER INFORMATION: Any amino acid
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60 <221> NAME/KEY: MOD_RES
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64 <220> FEATURE:
65 <221> NAME/KEY: MOD_RES

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TECH CENTER 1600/2900

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DEC 19 2001
TECH CENTER 1600/2900

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67 <223> OTHER INFORMATION: Any amino acid
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      121 1 5 10 15
W--> 123 Xaa Cys Xaa Xaa Cys Lys Xaa Phe Phe Xaa Arg Xaa Xaa Xaa Xaa
      124 20 25 30
W--> 126 Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys
      127 35 40 45

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129 Xaa Xaa Xaa Lys Xaa Xaa Arg Xaa Xaa Cys Xaa Xaa Cys Arg Xaa Xaa
 130 50 55 60
 132 Lys Cys Xaa Xaa Xaa Gly Met
 133 65 70
 136 <210> SEQ ID NO: 2
 137 <211> LENGTH: 5
 138 <212> TYPE: PRT
 139 <213> ORGANISM: Artificial Sequence
 141 <220> FEATURE:
 142 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 143 peptide
 145 <400> SEQUENCE: 2
 146 Glu Gly Cys Lys Gly
 147 1 5
 150 <210> SEQ ID NO: 3
 151 <211> LENGTH: 5
 152 <212> TYPE: PRT
 153 <213> ORGANISM: Artificial Sequence
 155 <220> FEATURE:
 156 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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 159 <400> SEQUENCE: 3
 160 Gly Ser Cys Lys Val
 161 1 5
 164 <210> SEQ ID NO: 4
 165 <211> LENGTH: 2241
 166 <212> TYPE: DNA
 167 <213> ORGANISM: Artificial Sequence
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 171 VgEcR
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 174 <221> NAME/KEY: CDS
 175 <222> LOCATION: (1)..(2238)
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 179 Met Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp
 180 1 5 10 15
 182 ggc gag gac gtg gcg atg gcg cat gcc gac gcg cta gac gat ttc gat 96
 183 Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp
 184 20 25 30
 186 ctg gac atg ttg ggg gac ggg gat tcc ccg ggt ccg gga ttt acc ccc 144
 187 Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro
 188 35 40 45
 190 cac gac tcc gcc ccc tac ggc gct ctg gat atg gcc gac ttc gag ttt 192
 191 His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe
 192 50 55 60
 194 gag cag atg ttt acc gat gcc ctt gga att gac gag tac ggt ggg aag 240
 195 Glu Gln Met Phe Thr Asp Ala Leu Gly Ile Asp Glu Tyr Gly Gly Lys

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Input Set : A:\SA1520-2.APP.txt

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196	65		70		75		80	
198	ctt cta ggt acc tct aga agg ata tcg aat tct ata tct tca ggt cgc	288						
199	Leu Leu Gly Thr Ser Arg Arg Ile Ser Asn Ser Ile Ser Ser Gly Arg							
200		85		90		95		
202	gat gat ctg tcg cct tcg agc agc ttg aac gga tac tcg gcg aac gaa	336						
203	Asp Asp Leu Ser Pro Ser Ser Ser Leu Asn Gly Tyr Ser Ala Asn Glu							
204		100		105		110		
206	agc tgc gat gcg aag aag agc aag aag gga cct gcg cca cgg gtg caa	384						
207	Ser Cys Asp Ala Lys Lys Ser Lys Lys Gly Pro Ala Pro Arg Val Gln							
208		115		120		125		
210	gag gag ctg tgc ctg gtt tgc ggc gac agg gcc tcc ggc tac cac tac	432						
211	Glu Glu Leu Cys Leu Val Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr							
212		130		135		140		
214	aac gcc ctg acc tgt gga tcc tgc aag gtg ttc ttt cga cgc agc gtt	480						
215	Asn Ala Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Arg Arg Ser Val							
216	145		150		155		160	
218	acg aag agc gcc gtc tac tgc tgc aag ttc ggg cgc gcc tgc gaa atg	528						
219	Thr Lys Ser Ala Val Tyr Cys Cys Lys Phe Gly Arg Ala Cys Glu Met							
220		165		170		175		
222	gac atg tac atg agg cga aag tgt cag gag tgc cgc ctg aaa aag tgc	576						
223	Asp Met Tyr Met Arg Arg Lys Cys Gln Glu Cys Arg Leu Lys Lys Cys							
224		180		185		190		
226	ctg gcc gtg ggt atg cgg ccg gaa tgc gtc gtc ccg gag aac caa tgt	624						
227	Leu Ala Val Gly Met Arg Pro Glu Cys Val Val Pro Glu Asn Gln Cys							
228		195		200		205		
230	gcg atg aag cgg cgc gaa aag aag gcc cag aag gag aag gac aaa atg	672						
231	Ala Met Lys Arg Arg Glu Lys Lys Ala Gln Lys Glu Lys Asp Lys Met							
232		210		215		220		
234	acc act tcg ccg agc tct cag cat ggc ggc aat ggc agc ttg gcc tct	720						
235	Thr Thr Ser Pro Ser Ser Gln His Gly Gly Asn Gly Ser Leu Ala Ser							
236	225		230		235		240	
238	ggt ggc ggc caa gac ttt gtt aag aag gag att ctt gac ctt atg aca	768						
239	Gly Gly Gly Gln Asp Phe Val Lys Lys Glu Ile Leu Asp Leu Met Thr							
240		245		250		255		
242	tgc gag ccg ccc cag cat gcc act att ccg cta cta cct gat gaa ata	816						
243	Cys Glu Pro Pro Gln His Ala Thr Ile Pro Leu Leu Pro Asp Glu Ile							
244		260		265		270		
246	ttg gcc aag tgt caa gcg cgc aat ata cct tcc tta acg tac aat cag	864						
247	Leu Ala Lys Cys Gln Ala Arg Asn Ile Pro Ser Leu Thr Tyr Asn Gln							
248		275		280		285		
250	ttg gcc gtt ata tac aag tta att tgg tac cag gat ggc tat gag cag	912						
251	Leu Ala Val Ile Tyr Lys Leu Ile Trp Tyr Gln Asp Gly Tyr Glu Gln							
252		290		295		300		
254	cca tct gaa gag gat ctg agg cgt ata atg agt caa ccc gat gag aac	960						
255	Pro Ser Glu Glu Asp Leu Arg Arg Ile Met Ser Gln Pro Asp Glu Asn							
256	305		310		315		320	
258	gag agc caa acg gac gtc agc ttt cgg cat ata acc gag ata acc ata	1008						
259	Glu Ser Gln Thr Asp Val Ser Phe Arg His Ile Thr Glu Ile Thr Ile							
260		325		330		335		

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262 ctc acg gtc cag ttg att gtt gag ttt gct aaa ggt cta cca gcg ttt 1056
263 Leu Thr Val Gln Leu Ile Val Glu Phe Ala Lys Gly Leu Pro Ala Phe
264          340          345          350
266 aca aag ata ccc cag gag gac cag atc acg tta cta aag gcc tgc tcg 1104
267 Thr Lys Ile Pro Gln Glu Asp Gln Ile Thr Leu Leu Lys Ala Cys Ser
268          355          360          365
270 tcg gag gtg atg atg ctg cgt atg gca cga cgc tat gac cac agc tcg 1152
271 Ser Glu Val Met Met Leu Arg Met Ala Arg Arg Tyr Asp His Ser Ser
272          370          375          380
274 gac tca ata ttc ttc gcg aat aat aga tca tat acg cgg gat tct tac 1200
275 Asp Ser Ile Phe Phe Ala Asn Asn Arg Ser Tyr Thr Arg Asp Ser Tyr
276 385          390          395          400
278 aaa atg gcc gga atg gct gat aac att gaa gac ctg ctg cat ttc tgc 1248
279 Lys Met Ala Gly Met Ala Asp Asn Ile Glu Asp Leu Leu His Phe Cys
280          405          410          415
282 cgc caa atg ttc tcg atg aag gtg gac aac gtc gaa tac gcg ctt ctc 1296
283 Arg Gln Met Phe Ser Met Lys Val Asp Asn Val Glu Tyr Ala Leu Leu
284          420          425          430
286 act gcc att gtg atc ttc tcg gac cgg ccg ggc ctg gag aag gcc caa 1344
287 Thr Ala Ile Val Ile Phe Ser Asp Arg Pro Gly Leu Glu Lys Ala Gln
288          435          440          445
290 cta gtc gaa gcg atc cag agc tac tac atc gac acg cta cgc att tat 1392
291 Leu Val Glu Ala Ile Gln Ser Tyr Tyr Ile Asp Thr Leu Arg Ile Tyr
292          450          455          460
294 ata ctc aac cgc cac tgc ggc gac tca atg agc ctc gtc ttc tac gca 1440
295 Ile Leu Asn Arg His Cys Gly Asp Ser Met Ser Leu Val Phe Tyr Ala
296 465          470          475          480
298 aag ctg ctc tcg atc ctc acc gag ctg cgt acg ctg ggc aac cag aac 1488
299 Lys Leu Leu Ser Ile Leu Thr Glu Leu Arg Thr Leu Gly Asn Gln Asn
300          485          490          495
302 gcc gag atg tgt ttc tca cta aag ctc aaa aac cgc aaa ctg ccc aag 1536
303 Ala Glu Met Cys Phe Ser Leu Lys Leu Lys Asn Arg Lys Leu Pro Lys
304          500          505          510
306 ttc ctc gag gag atc tgg gac gtt cat gcc atc ccg cca tcg gtc cag 1584
307 Phe Leu Glu Glu Ile Trp Asp Val His Ala Ile Pro Pro Ser Val Gln
308          515          520          525
310 tcg cac ctt cag att acc cag gag gag aac gag cgt ctc gag cgg gct 1632
311 Ser His Leu Gln Ile Thr Gln Glu Glu Asn Glu Arg Leu Glu Arg Ala
312          530          535          540
314 gag cgt atg cgg gca tcg gtt ggg ggc gcc att acc gcc ggc att gat 1680
315 Glu Arg Met Arg Ala Ser Val Gly Gly Ala Ile Thr Ala Gly Ile Asp
316 545          550          555          560
318 tgc gac tct gcc tcc act tcg gcg gcg gca gcc gcg gcc cag cat cag 1728
319 Cys Asp Ser Ala Ser Thr Ser Ala Ala Ala Ala Ala Ala Gln His Gln
320          565          570          575
322 cct cag cct cag ccc cag ccc caa ccc tcc tcc ctg acc cag aac gat 1776
323 Pro Gln Pro Gln Pro Gln Pro Gln Pro Ser Ser Leu Thr Gln Asn Asp
324          580          585          590
326 tcc cag cac cag aca cag ccg cag cta caa cct cag cta cca cct cag 1824

```

Use of n and/or Xaa has been detected in the Sequence Listing.

→ Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY

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L:120 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:123 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:126 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:129 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:132 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:1387 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:1417 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1435 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:1465 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13